

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Jun 07 17:57:20 EDT 2007

=====

Application No: 10728979

Version No: 1.0

Input Set:**Output Set:****Started:** 2007-06-07 09:28:31.766**Finished:** 2007-06-07 09:28:33.424**Elapsed:** 0 hr(s) 0 min(s) 1 sec(s) 658 ms**Total Warnings:** 38**Total Errors:** 0**No. of SeqIDs Defined:** 93**Actual SeqID Count:** 93

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)

Input Set:

Output Set:

Started: 2007-06-07 09:28:31.766
Finished: 2007-06-07 09:28:33.424
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 658 ms
Total Warnings: 38
Total Errors: 0
No. of SeqIDs Defined: 93
Actual SeqID Count: 93

Error code

Error Description

This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> NEC CORPORATION
 MIYAKAWA, Tomoya
 NAKAZATO, Takeru
 ASOGAWA, Minoru

<120> Sequence Display Method and Homogeny Search Method

<130> Q78853

<140> 10728979

<141> 2007-06-07

<150> JP 2002-358407

<151> 2002-12-10

<150> US 10/728,979

<151> 2003-12-08

<160> 93

<170> PatentIn version 3.1

<210> 1

<211> 1560

<212> DNA

<213> Artificial Sequence

<220>

<223> QUERY Polynucleotide

<220>

<221> CDS

<222> (1)..(1560)

<400> 1

atg act gag ctg aag gca aag ggt ccc cgg gct ccc cac gtg gcg ggc	48
Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly	
1 5 10 15	

ggc cgg ccc tcc ccc gag gtc gga tcc cca ctg ctg tgt cgc cca gcc	96
Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala	
20 25 30	

gca ggt ccg ttc ccg ggg agc cag acc tcg gac acc ttg cct gaa gtt	144
Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val	
35 40 45	

tcg gcc ata cct atc tcc ctg gac ggg cta ctc ttc cct cgg ccc tgc	192
Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys	
50 55 60	

cag gga cag gac ccc tcc gac gaa aag acg cag gac cag cag tcg ctg	240
Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu	
65 70 75 80	

tcg gac gtg gag ggc gca tat tcc aga gct gaa gct aca agg ggt gct	288
Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala	
85 90 95	
gga ggc agc agt tct agt ccc cca gaa aag gac agc gga ctg ctg gac	336
Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp	
100 105 110	
agt gtc ttg gac act ctg ttg gcg ccc tca ggt ccc ggg cag agc caa	384
Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln	
115 120 125	
ccc agc cct ccc gcc tgc gag gtc acc agc tct tgg tgc ctg ttt ggc	432
Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly	
130 135 140	
ccc gaa ctt ccc gaa gat cca ccg gct gcc ccc gcc acc cag cgg gtg	480
Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val	
145 150 155 160	
ttg tcc ccg ctc atg agc cgg tcc ggg tgc aag gtt gga gac agc tcc	528
Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser	
165 170 175	
ggg acg gca gct gcc cat aaa gtg ctg ccc cgg ggc ctg tca cca gcc	576
Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala	
180 185 190	
cgg cag ctg ctg ctc ccg gcc tct gag agc cct cac tgg tcc ggg gcc	624
Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala	
195 200 205	
cca gtg aag ccg tct ccg cag gcc gct gcg gtg gag gtt gag gag gag	672
Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu	
210 215 220	
gat agc tct gag tcc gag gag tct gcg ggt ccg ctt ctg aag ggc aaa	720
Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys	
225 230 235 240	
cct cgg gct ctg ggt ggc gcg gcg gct gga gga gga gcc gcg gct tgt	768
Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Cys	
245 250 255	
ccg ccg ggg gcg gca gca gga ggc gtc gcc ctg gtc ccc aag gaa gat	816
Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp	
260 265 270	
tcc cgc ttc tca gcg ccc agg gtc gcc ctg gtg gag cag gac gcg ccg	864
Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro	
275 280 285	
atg gcg ccc ggg cgc tcc ccg ctg gcc acc acg gtg atg gat ttc atc	912
Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile	
290 295 300	
cac gtg cct atc ctg cct ctc aat cac gcc tta ttg gca gcc cgc act	960

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr	
305	310 315 320
cgg cag ctg ctg gaa gac gaa agt tac gac ggc ggg gcc ggg gct gcc	1008
Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala	
325 330 335	
agc gcc ttt gcc ccg ccg cgg act tca ccc tgt gcc tcg tcc acc ccg	1056
Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro	
340 345 350	
gtc gct gta ggc gac ttc ccc gac tgc gcg tac ccg ccc gac gcc gag	1104
Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu	
355 360 365	
ccc aag gac gac gcg tac cct ctc tat agc gac ttc cag ccg ccc gct	1152
Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala	
370 375 380	
cta aag ata aag gag gag gag gaa ggc gcg gag gcc tcc gcg cgc tcc	1200
Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser	
385 390 395 400	
ccg cgt tcc tac ctt gtg gcc ggt gcc aac ccc gca gcc ttc ccg gat	1248
Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp	
405 410 415	
ttc ccg ttg ggg cca ccg ccc ccg ctg ccg ccg cga gcg acc cca tcc	1296
Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser	
420 425 430	
aga ccc ggg gaa gcg gcg gtg acg gcc gca ccc gcc agt gcc tca gtc	1344
Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val	
435 440 445	
tcg tct gcg tcc tcc tcg ggg tcg acc ctg gag tgc atc ctg tac aaa	1392
Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys	
450 455 460	
gcg gag ggc gcg ccg ccc cag cag ggc ccg ttc gcg ccg ccg ccc tgc	1440
Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys	
465 470 475 480	
aag gcg ccg ggc gcg agc ggc tgc ctg ctc ccg cgg gac ggc ctg ccc	1488
Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro	
485 490 495	
tcc acc tcc gcc tct gcc gcc gcc gcc ggg gcg gcc ccc gcg ctc tac	1536
Ser Thr Ser Ala Ser Ala Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr	
500 505 510	
cct gca ctc ggc ctc aac ggg ctc	1560
Pro Ala Leu Gly Leu Asn Gly Leu	
515 520	

<211> 520
<212> PRT
<213> Artificial Sequence

<220>
<223> QUERY Polypeptide

<400> 2

Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly
1 5 10 15

Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
20 25 30

Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Gly Ala Ala Ala Cys
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser

420

425

430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu
515 520

<210> 3

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> QUERY 1-60 Polynucleotide

<400> 3

atgactgagc tgaaggcaaa gggccccgg gctccccacg tggcgggcgg cccgcctcc 60

<210> 4

<211> 57

<212> DNA

<213> Unknown Sequence

<220>

<223> gn1|dbSNP|rs2008112 polynucleotide

<400> 4

atgactgagc tgaggcaaag ggtccccgg ctcccacgtg gcgggcggcc gcccttc 57

<210> 5

<211> 60

<212> DNA

<213> artificial

<220>

<223> gi|35651|emb|X51730.1|HSPREC

<400> 5

atgactgagc tgaaggcaaa ggggtccccgg gctccccacg tggcgggcgg cccgccctcc 60

<210> 6

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|4102792|gb|AF016381.1|AF016381 Polynucleotide

<400> 6

atgactgagc tgaaggcaaa ggggtccccgg gctccccacg tggcgggcgg cccgccctcc 60

<210> 7

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|4505766|ref|NM Polynucleotide

<400> 7

atgactgagc tgaaggcaaa ggggtccccgg gctccccacg tggcgggcgg cccgccctcc 60

<210> 8

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|189934|gb|M15716.1|HUMPGRG Polynucleotide

<400> 8

atgactgagc tgaaggcaaa ggggtccccgg gctccccacg tggcgggcgg cccgccctcc 60

<210> 9

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|22759951|dbj|AB085845.1| Polynucleotide

<400> 9

atgactgagc tgaaggcaaa ggggtccccgg gctccccacg tggcgggcgg cccgccctcc 60

<210> 10

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|22759949|dbj|AB085844.1| Polynucleotide

<400> 10
atgactgagc tgaaggcaaa gggtecccg gctccccacg tggcgggcgg cccgccctcc 60

<210> 11
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<223> gi|22036116|dbj|AB085683.1| Polynucleotide

<400> 11
atgactgagc tgaaggcaaa gggtecccg gctccccacg tggcgggcgg cccgccctcc 60

<210> 12
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<223> gi|20278870|dbj|AB084248.1| Polynucleotide

<400> 12
atgactgagc tgaaggcaaa gggtecccg gctccccacg tggcgggcgg cccgccctcc 60

<210> 13
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<223> gi|22759947|dbj|AB085843.1| Polynucleotide

<400> 13
atgactgagc tgaaggcaaa gggtecccg gctccccacg tggcgggcgg cccgccctcc 60

<210> 14
<211> 60
<212> DNA
<213> Artificial Sequence

<220>

<223> gi|14245763|dbj|AP001533.4| Polynucleotide

<400> 14
atgactgagc tgaaggcaaa gggtecccg gctccccacg tggcgggcgg cccgccctcc 60

<210> 15
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> QUERY 1801-1860 Polynucleotide

<400> 15
tacttatgtg ctggaagaaa tgactgcatc gttgataaaa tccgcagaaa aaactgccca 60

<210> 16
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> gi|19692498|emb|AL709143.1|AL709143 Polynucleotide

<400> 16
tacttatgtg ctggaagaaa tgactgcatc gttgataaaa tccgcagaaa aaactgccca 60

<210> 17
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> gi|15938608|gb|BI827058.1|BI827058 Polynucleotide

<400> 17
tacttatgtg ctggaagaaa tgactgcatc gttgataaaa tccgcagaaa aaactgcccg 60

<210> 18
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> gi|15943587|gb|BI832037.1|BI832037 Polynucleotide

<400> 18
tacttatgtg ctggaagaaa tgactgcatc gttgataaaa tccgcagaaa aaactgcccg 60

<210> 19
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> gi|22921092|gb|BU570792.1|BU570792 Polynucleotide

<400> 19

tacttatgtg ctggaagaaa tgactgcatc gttgataaaa tccgcagaaa aaactgccca 60

<210> 20

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|24718432|gb|CA388844.1|CA388844 Polynucleotide

<400> 20

tacctatgtg ctggaaggaa tgattgcatc atcgataaaa ttcgaagaaa aaactgccca 60

<210> 21

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|24117946|gb|BU929216.1|BU929216 Polynucleotide

<400> 21

tacctatgtg ctggaaggaa tgattgcatc atcgataaaa ttcgaagaaa aaactgccca 60

<210> 22

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|14002248|gb|BG723061.1|BG723061 Polynucleotide

<400> 22

tacctatgtg ctggaaggaa tgattgcatc atcgataaaa ttcgaagaaa aaactgccca 60

<210> 23

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|11005321|dbj|AU143800.1|AU143800 Polynucleotide

<400> 23

tacctatgtg ctggaaggaa tgattgcatc atcgataaaa ttcgaagaaa aaactgccca 60

<210> 24

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|9868500|dbj|AV647486.1|AV647486 Polynucleotide

<400> 24

tacctatgtg ctggaaggaa tgattgcatc atcgataaaa ttcgaagaaa aaactgccca 60

<210> 25

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|9868497|dbj|AV647483.1|AV647483 Polynucleotide

<400> 25

tacctatgtg ctggaaggaa tgattgcatc atcgataaaa ttcgaagaaa aaactgccca 60

<210> 26

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|9868443|dbj|AV647429.1|AV647429 Polynucleotide

<400> 26

tacctatgtg ctggaaggaa tgattgcatc atcgataaaa ttcgaagaaa aaactgccca 60

<210> 27

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> gi|4687594|gb|AI636264.1|AI636264 Polynucleotide

<400> 27

tacctatgtg ctggaaggaa tgattgcatc atcgataaaa ttcgaagaaa aaactgccca 6